



## SEQUENCE LISTING

<110> Yanofsky, Martin F.  
Liljegren, Sarah  
Ferrandiz, Cristina  
The Regents of the University of California

<120> Selective Control of Lignin Biosynthesis in Transgenic Plants

<130> 19452A-000940US

<140> US 09/981,087  
<141> 2001-10-15

<150> US 60/090,649  
<151> 1998-06-25

<150> US 09/339,998  
<151> 1999-06-25

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<170> PatentIn Ver. 2.1

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Met Gly Arg Gly Arg  
1 5  
ggt cag ctg aag agg ata gag aac aag atc aat agg caa gtt act ttc 163  
Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe  
10 15 20  
tca aag aga agg tct ggt ttg ctc aag aaa gct cat gag atc tct gtt 211  
Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala His Glu Ile Ser Val  
25 30 35  
ctc tgc gat gct gag gtt gct ctc atc gtc ttc tct tcc aaa ggc aaa 259  
Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe Ser Ser Lys Gly Lys  
40 45 50  
ctc ttc gaa tat tcc acc gac tct tgc atg gag agg ata ctt gaa cgc 307  
Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu Arg Ile Leu Glu Arg  
55 60 65  
tat gat cgc tat tta tat tca gac aaa caa ctt gtt ggc cga gac gtt 355  
Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu Val Gly Arg Asp Val  
70 75 80 85

tca caa agt gaa aat tgg gtt cta gaa cat gct aag ctc aag gca aga 403  
 Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala Lys Leu Lys Ala Arg  
 90 95 100  
 gtt gag gta ctt gag aag aac aaa agg aat ttt atg ggg gaa gat ctt 451  
 Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe Met Gly Glu Asp Leu  
 105 110 115  
 gat tcg ttg agc ttg aag gag ctc caa agc ttg gag cat cag ctc gat 499  
 Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu Glu His Gln Leu Asp  
 120 125 130  
 gca gct atc aag agc att agg tca aga aag aac caa gct atg ttc gaa 547  
 Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn Gln Ala Met Phe Glu  
 135 140 145  
 tcc ata tct gcg ctc cag aag aag gat aaa gcc ttg caa gat cac aac 595  
 Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala Leu Gln Asp His Asn  
 150 155 160 165  
 aat tcg ctt ctc aaa aag att aag gag agg gag aag aaa acg ggt cag 643  
 Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu Lys Lys Thr Gly Gln  
 170 175 180  
 caa gaa gga caa tta gtc caa tgc tcc aac tct tct tca gtt ctt ctg 691  
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 Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly Phe Val Glu Arg Val  
 200 205 210  
 ggg gga gag aac ggt ggt gca tcg tcg ttg acg gaa cca aac tct ctg 787  
 Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr Glu Pro Asn Ser Leu  
 215 220 225  
 ctt ccg gct tgg atg tta cgt cct acc act acg aac gag tag 829  
 Leu Pro Ala Trp Met Leu Arg Pro Thr Thr Asn Glu  
 230 235 240  
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&lt;212&gt; PRT

&lt;213&gt; Arabidopsis sp.

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 20 25 30  
 His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Val Phe  
 35 40 45

Ser Ser Lys Gly Lys Leu Phe Glu Tyr Ser Thr Asp Ser Cys Met Glu  
 50 55 60  
 Arg Ile Leu Glu Arg Tyr Asp Arg Tyr Leu Tyr Ser Asp Lys Gln Leu  
 65 70 75 80  
 Val Gly Arg Asp Val Ser Gln Ser Glu Asn Trp Val Leu Glu His Ala  
 85 90 95  
 Lys Leu Lys Ala Arg Val Glu Val Leu Glu Lys Asn Lys Arg Asn Phe  
 100 105 110  
 Met Gly Glu Asp Leu Asp Ser Leu Ser Leu Lys Glu Leu Gln Ser Leu  
 115 120 125  
 Glu His Gln Leu Asp Ala Ala Ile Lys Ser Ile Arg Ser Arg Lys Asn  
 130 135 140  
 Gln Ala Met Phe Glu Ser Ile Ser Ala Leu Gln Lys Lys Asp Lys Ala  
 145 150 155 160  
 Leu Gln Asp His Asn Asn Ser Leu Leu Lys Lys Ile Lys Glu Arg Glu  
 165 170 175  
 Lys Lys Thr Gly Gln Gln Glu Gly Gln Leu Val Gln Cys Ser Asn Ser  
 180 185 190  
 Ser Ser Val Leu Leu Pro Gln Tyr Cys Val Thr Ser Ser Arg Asp Gly  
 195 200 205  
 Phe Val Glu Arg Val Gly Gly Glu Asn Gly Gly Ala Ser Ser Leu Thr  
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<222> (7)..(753)

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 Lys Leu Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu Asn Thr Thr  
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 aat cgt caa gtt act ttc tgc aaa cga cgc aat ggt ctt ctc aag aaa 144  
 Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu Leu Lys Lys  
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 gct tat gaa ctc tct gtc ttg tgt gat gcc gaa gtt gcc ctc gtc atc 192  
 Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile  
 50 55 60  
 ttc tcc act cgt ggc cgt ctc tat gag tac gcc aac aac agt gtg agg 240  
 Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg  
 65 70 75  
 ggt aca att gaa agg tac aag aaa gct tgt tcc gat gcc gtc aac cct 288  
 Gly Thr Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro  
 80 85 90

cct tcc gtc acc gaa gct aat act cag tac tat cag caa gaa gcc tct 336  
 Pro Ser Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser  
 95 100 105 110  
 aag ctt cgg agg cag att cga gat att cag aat tca aat agg cat att 384  
 Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile  
 115 120 125  
 gtt ggg gaa tca ctt ggt tcc ttg aac ttc aag gaa ctc aaa aac cta 432  
 Val Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu  
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 Glu Gly Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn  
 145 150 155  
 gag ctg tta gtg gca gag ata gag tat atg cag aag agg gaa atg gag 528  
 Glu Leu Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg Glu Met Glu  
 160 165 170  
 ttg caa cac aat aac atg tac ctg cga gca aag ata gcc gaa ggc gcc 576  
 Leu Gln His Asn Asn Met Tyr Leu Arg Ala Lys Ile Ala Glu Gly Ala  
 175 180 185 190  
 aga ttg aat ccg gac cag cag gaa tcg agt gtg ata caa ggg acg aca 624  
 Arg Leu Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr  
 195 200 205  
 gtt tac gaa tcc ggt gta tct tct cat gac cag tcg cag cat tat aat 672  
 Val Tyr Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn  
 210 215 220  
 cgg aac tat att ccg gtg aac ctt ctt gaa ccg aat cag caa ttc tcc 720  
 Arg Asn Tyr Ile Pro Val Asn Leu Leu Glu Pro Asn Gln Gln Phe Ser  
 225 230 235  
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 Gly Gln Asp Gln Pro Pro Leu Gln Leu Val  
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 ttcttccct cataacgatt aagagagaga cgagagagtt cattttatat ttataacgcg 833  
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 35 40 45  
 Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Val Ile Phe Ser  
 50 55 60

Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn Ser Val Arg Gly Thr  
 65 70 75 80  
 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Ser  
 85 90 95  
 Val Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln Glu Ala Ser Lys Leu  
 100 105 110  
 Arg Arg Gln Ile Arg Asp Ile Gln Asn Ser Asn Arg His Ile Val Gly  
 115 120 125  
 Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu Lys Asn Leu Glu Gly  
 130 135 140  
 Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser Lys Lys Asn Glu Leu  
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 Asn Pro Asp Gln Gln Glu Ser Ser Val Ile Gln Gly Thr Thr Val Tyr  
 195 200 205  
 Glu Ser Gly Val Ser Ser His Asp Gln Ser Gln His Tyr Asn Arg Asn  
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 agc agc aag aag ata ggg aga ggg aag ata gag ata aag agg ata gag 158  
 Ser Ser Lys Lys Ile Gly Arg Gly Lys Ile Glu Ile Lys Arg Ile Glu  
 15 20 25  
 aac act acg aat cgt caa gtc act ttc tgc aaa cga cgc aat ggt tta 206  
 Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg Asn Gly Leu  
 30 35 40  
 ctc aag aaa gct tat gag ctc tct gtc ttg tgt gac gct gag gtt gct 254  
 Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala  
 45 50 55  
 ctt gtc atc ttc tcc act cga ggc cgt ctc tac gag tac gcc aac aac 302  
 Leu Val Ile Phe Ser Thr Arg Gly Arg Leu Tyr Glu Tyr Ala Asn Asn  
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agt gtg aga gga aca ata gaa agg tac aag aaa gct tgc tcc gac gcc 350
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ggt aac cct ccg acc atc acc gaa gct aat act cag tac tat cag caa 398
Val Asn Pro Pro Thr Ile Thr Glu Ala Asn Thr Gln Tyr Tyr Gln Gln
      95                      100                      105

gag gcg tct aaa ctc cgg aga cag att cgg gac att cag aat ttg aac 446
Glu Ala Ser Lys Leu Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn
     110                      115                      120

aga cac att ctt ggt gaa tct ctt ggt tcc ttg aac ttt aag gaa ctc 494
Arg His Ile Leu Gly Glu Ser Leu Gly Ser Leu Asn Phe Lys Glu Leu
     125                      130                      135

aag aac ctt gaa agt agg ctt gag aaa gga atc agt cgt gtc cga tcc 542
Lys Asn Leu Glu Ser Arg Leu Glu Lys Gly Ile Ser Arg Val Arg Ser
    140                      145                      150                      155

aag aag cac gag atg tta gtt gca gag att gaa tac atg caa aaa agg 590
Lys Lys His Glu Met Leu Val Ala Glu Ile Glu Tyr Met Gln Lys Arg
     160                      165                      170

gaa atc gag ctg caa aac gat aac atg tat ctc cgc tcc aag att act 638
Glu Ile Glu Leu Gln Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr
     175                      180                      185

gaa aga aca ggt cta cag caa caa gaa tcg agt gtg ata cat caa ggg 686
Glu Arg Thr Gly Leu Gln Gln Gln Glu Ser Ser Val Ile His Gln Gly
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aca gtt tac gag tcg ggt gtt act tct tct cac cag tcg ggg cag tat 734
Thr Val Tyr Glu Ser Gly Val Thr Ser Ser His Gln Ser Gly Gln Tyr
     205                      210                      215

aac cgg aat tat att gcg gtt aac ctt ctt gaa ccg aat cag aat tcc 782
Asn Arg Asn Tyr Ile Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser
    220                      225                      230                      235

tcc aac caa gac caa cca cct ctg caa ctt gtt tga ttcagtctaa 828
Ser Asn Gln Asp Gln Pro Pro Leu Gln Leu Val
     240                      245

cataagcttc tttcctcagc ctgagatcga tctatagtgt cacctaaatg cggccgcgtc 888

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           50                          55                          60  
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 Ile Glu Arg Tyr Lys Lys Ala Cys Ser Asp Ala Val Asn Pro Pro Thr  
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 Arg Arg Gln Ile Arg Asp Ile Gln Asn Leu Asn Arg His Ile Leu Gly  
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 Asn Asp Asn Met Tyr Leu Arg Ser Lys Ile Thr Glu Arg Thr Gly Leu  
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           210                          215                          220  
 Ala Val Asn Leu Leu Glu Pro Asn Gln Asn Ser Ser Asn Gln Asp Gln  
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27

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 <212> DNA  
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&lt;221&gt; CDS

&lt;222&gt; (2758)..(3354)

<223> R-like basic heix-loop-helix transcription factor  
(R-like bHLH)

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                   35                  40                  45  
 Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met  
                   50                  55                  60  
 Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu  
   65                  70                  75                  80

Tyr	Asp	Glu	Asp	Met	Asp	Ala	Met	Lys	Glu	Met	Gln	Tyr	Met	Ile	Ala	85	90	95
Val	Met	Gln	Pro	Val	Asp	Ile	Asp	Pro	Ala	Thr	Val	Pro	Lys	Pro	Asn	100	105	110
Arg	Arg	Asn	Val	Arg	Ile	Ser	Asp	Asp	Pro	Gln	Thr	Val	Val	Ala	Arg	115	120	125
Arg	Arg	Arg	Glu	Arg	Ile	Ser	Glu	Lys	Ile	Arg	Ile	Leu	Lys	Arg	Ile	130	135	140
Val	Pro	Gly	Gly	Ala	Lys	Met	Asp	Thr	Ala	Ser	Met	Leu	Asp	Glu	Ala	145	150	155
Ile	Arg	Tyr	Thr	Lys	Phe	Leu	Lys	Arg	Gln	Val	Arg	Ile	Leu	Gln	Pro	165	170	175
His	Ser	Gln	Ile	Gly	Ala	Pro	Met	Ala	Asn	Pro	Ser	Tyr	Leu	Cys	Tyr	180	185	190
Tyr	His	Asn	Ser	Gln	Pro											195		